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WO 02/26950 A2

(54) Title: **TRANSFERASES**

(57) **Abstract:** The invention provides human transferases (TRNFR) and polynucleotides which identify and encode TRNFR. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with aberrant expression of TRNFR.

	245		250		255
Gly Lys His Phe Trp Ser Phe Gln Met Tyr Gly Glu Asp Phe Val					
	260		265		270
Pro Asp Ile Val Thr Met Gly Lys Pro Met Gly Asn Gly His Pro					
	275		280		285
Val Ala Cys Val Val Thr Thr Lys Glu Ile Ala Glu Ala Phe Ser					
	290		295		300
Ser Ser Gly Met Glu Tyr Phe Asn Thr Tyr Gly Gly Asn Pro Val					
	305		310		315
Ser Cys Ala Val Gly Leu Ala Val Leu Asp Ile Ile Glu Asn Glu					
	320		325		330
Asp Leu Gln Gly Asn Ala Lys Arg Val Gly Asn Tyr Leu Thr Glu					
	335		340		345
Leu Leu Lys Lys Gln Lys Ala Lys His Thr Leu Ile Gly Asp Ile					
	350		355		360
Arg Gly Ile Gly Leu Phe Ile Gly Ile Asp Leu Val Lys Asp His					
	365		370		375
Leu Lys Arg Thr Pro Ala Thr Ala Glu Ala Gln His Ile Ile Tyr					
	380		385		390
Lys Met Lys Glu Lys Arg Val Leu Leu Ser Ala Asp Gly Pro His					
	395		400		405
Arg Asn Val Leu Lys Ile Lys Pro Pro Met Cys Phe Thr Glu Glu					
	410		415		420
Asp Ala Lys Phe Met Val Asp Gln Leu Asp Arg Ile Leu Thr Val					
	425		430		435
Leu Glu Glu Ala Met Gly Thr Lys Thr Glu Ser Val Thr Ser Glu					
	440		445		450
Asn Thr Pro Cys Lys Thr Lys Met Leu Lys Glu Ala His Ile Glu					
	455		460		465
Leu Leu Arg Asp Ser Thr Thr Asp Ser Lys Glu Asn Pro Ser Arg					
	470		475		480
Lys Arg Asn Gly Met Cys Thr Asp Thr His Ser Leu Leu Ser Lys					
	485		490		495
Arg Leu Lys Thr					

&lt;210&gt; 14

&lt;211&gt; 721

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: 2124971CD1

&lt;400&gt; 14

Met Leu Pro Arg Gly Arg Pro Arg Ala Leu Gly Ala Ala Ala Leu			
1	5	10	15
Leu Leu Leu Leu Leu Leu Leu Gly Phe Leu Leu Phe Gly Gly Asp			
	20	25	30
Leu Gly Cys Glu Arg Arg Glu Pro Gly Gly Arg Ala Gly Ala Pro			
	35	40	45
Gly Cys Phe Pro Gly Pro Leu Met Pro Arg Val Pro Pro Asp Gly			
	50	55	60
Arg Leu Arg Arg Ala Ala Ala Leu Asp Gly Asp Pro Gly Ala Gly			
	65	70	75

Pro Gly Asp His	Asn Arg Ser Asp Cys	Gly Pro Gln Pro Pro	Pro
80		85	90
Pro Pro Lys Cys	Glu Leu Leu His Val	Ala Ile Val Cys Ala Gly	
95		100	105
His Asn Ser Ser	Arg Asp Val Ile Thr	Leu Val Lys Ser Met Leu	
110		115	120
Phe Tyr Arg Lys	Asn Pro Leu His Leu	His Leu Val Thr Asp Ala	
125		130	135
Val Ala Arg Asn	Ile Leu Glu Thr Leu	Phe His Thr Trp Met Val	
140		145	150
Pro Ala Val Arg	Val Ser Phe Tyr His	Ala Asp Gln Leu Lys Pro	
155		160	165
Gln Val Ser Trp	Ile Pro Asn Lys His	Tyr Ser Gly Leu Tyr Gly	
170		175	180
Leu Met Lys Leu	Val Leu Pro Ser Ala	Leu Pro Ala Glu Leu Ala	
185		190	195
Arg Val Ile Val	Leu Asp Thr Asp Val	Thr Phe Ala Ser Asp Ile	
200		205	210
Ser Glu Leu Trp	Ala Leu Phe Ala His	Phe Ser Asp Thr Gln Ala	
215		220	225
Ile Gly Leu Val	Glu Asn Gln Ser Asp	Trp Tyr Leu Gly Asn Leu	
230		235	240
Trp Lys Asn His	Arg Pro Trp Pro Ala	Leu Gly Arg Gly Phe Asn	
245		250	255
Thr Gly Val Ile	Leu Leu Arg Leu Asp	Arg Leu Arg Gln Ala Gly	
260		265	270
Trp Glu Gln Met	Trp Arg Leu Thr Ala	Arg Arg Glu Leu Leu Ser	
275		280	285
Leu Pro Ala Thr	Ser Leu Ala Asp Gln	Asp Ile Phe Asn Ala Val	
290		295	300
Ile Lys Glu His	Pro Gly Leu Val Gln	Arg Leu Pro Cys Val Trp	
305		310	315
Asn Val Gln Leu	Ser Asp His Thr Leu	Ala Glu Arg Cys Tyr Ser	
320		325	330
Glu Ala Ser Asp	Leu Lys Val Ile His	Trp Asn Ser Pro Lys Lys	
335		340	345
Leu Arg Val Lys	Asn Lys His Val Glu	Phe Phe Arg Asn Phe Tyr	
350		355	360
Leu Thr Phe Leu	Glu Tyr Asp Gly Asn	Leu Leu Arg Arg Glu Leu	
365		370	375
Phe Val Cys Pro	Ser Gln Pro Pro Pro	Gly Ala Glu Gln Leu Gln	
380		385	390
Gln Ala Leu Ala	Gln Leu Asp Glu Glu	Asp Pro Cys Phe Glu Phe	
395		400	405
Arg Gln Gln Gln	Leu Thr Val His Arg	Val His Val Thr Phe Leu	
410		415	420
Pro His Glu Pro	Pro Pro Arg Pro	His Asp Val Thr Leu Val	
425		430	435
Ala Gln Leu Ser	Met Asp Arg Leu Gln	Met Leu Glu Ala Leu Cys	
440		445	450
Arg His Trp Pro	Gly Pro Met Ser Leu	Ala Leu Tyr Leu Thr Asp	
455		460	465
Ala Glu Ala Gln	Gln Phe Leu His Phe	Val Glu Ala Ser Pro Val	
470		475	480
Leu Ala Ala Arg	Gln Asp Val Ala Tyr	His Val Val Tyr Arg Glu	
485		490	495

Gly Pro Leu Tyr Pro Val Asn Gln Leu Arg Asn Val Ala Leu Ala  
 500 505 510  
 Gln Ala Leu Thr Pro Tyr Val Phe Leu Ser Asp Ile Asp Phe Leu  
 515 520 525  
 Pro Ala Tyr Ser Leu Tyr Asp Tyr Leu Arg Ala Ser Ile Glu Gln  
 530 535 540  
 Leu Gly Leu Gly Ser Arg Arg Lys Ala Ala Leu Val Val Pro Ala  
 545 550 555  
 Phe Glu Thr Leu Arg Tyr Arg Phe Ser Phe Pro His Ser Lys Val  
 560 565 570  
 Glu Leu Leu Ala Leu Leu Asp Ala Gly Thr Leu Tyr Thr Phe Arg  
 575 580 585  
 Tyr His Glu Trp Pro Arg Gly His Ala Pro Thr Asp Tyr Ala Arg  
 590 595 600  
 Trp Arg Glu Ala Gln Ala Pro Tyr Arg Val Gln Trp Ala Ala Asn  
 605 610 615  
 Tyr Glu Pro Tyr Val Val Val Pro Arg Asp Cys Pro Arg Tyr Asp  
 620 625 630  
 Pro Arg Phe Val Gly Phe Gly Trp Asn Lys Val Ala His Ile Val  
 635 640 645  
 Glu Leu Asp Ala Gln Glu Tyr Glu Leu Leu Val Leu Pro Glu Ala  
 650 655 660  
 Phe Thr Ile His Leu Pro His Ala Pro Ser Leu Asp Ile Ser Arg  
 665 670 675  
 Phe Arg Ser Ser Pro Thr Tyr Arg Asp Cys Leu Gln Ala Leu Lys  
 680 685 690  
 Asp Glu Phe His Gln Asp Leu Ser Arg His His Gly Ala Ala Ala  
 695 700 705  
 Leu Lys Tyr Leu Pro Ala Leu Gln Gln Pro Gln Ser Pro Ala Arg  
 710 715 720  
 Gly

&lt;210&gt; 15

&lt;211&gt; 552

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte ID No: 2258250CD1

&lt;400&gt; 15

Met Ala Asn Pro Gly Gly Gly Ala Val Cys Asn Gly Lys Leu His  
 1 5 10 15  
 Asn His Lys Lys Gln Ser Asn Gly Ser Gln Ser Arg Asn Cys Thr  
 20 25 30  
 Lys Asn Gly Ile Val Lys Glu Ala Gln Gln Asn Gly Lys Pro His  
 35 40 45  
 Phe Tyr Asp Lys Leu Ile Val Glu Ser Phe Glu Glu Ala Pro Leu  
 50 55 60  
 His Val Met Val Phe Thr Tyr Met Gly Tyr Gly Ile Gly Thr Leu  
 65 70 75  
 Phe Gly Tyr Leu Arg Asp Phe Leu Arg Asn Trp Gly Ile Glu Lys  
 80 85 90  
 Cys Asn Ala Ala Val Glu Arg Lys Glu Gln Lys Asp Phe Val Pro

AAE22152  
 ID AAE22152 standard; Protein; 721 AA.  
 XX  
 AC AAE22152;  
 XX  
 DT 25-JUL-2002 (first entry)  
 XX  
 DE Human TRNFR-14 protein.  
 XX  
 PN WO200226950-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PF 28-SEP-2001; 2001WO-US30424.  
 XX  
 PR 29-SEP-2000; 2000US-236523P.  
 PR 06-OCT-2000; 2000US-238481P.  
 PR 27-OCT-2000; 2000US-244025P.  
 PR 03-NOV-2000; 2000US-246001P.  
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 PR 16-NOV-2000; 2000US-249639P.  
 PR 21-NOV-2000; 2000US-252819P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 PI Lal PG, Tang YT, Yue H, Burford N, Gandhi AR, Warren BA, Yao MG;  
 PI Tribouley CM, Baughn MR, Lee EA, Hafalia AJA, Lu Y, Griffin JA;  
 PI Sanjanwala MS, Ding L;  
 XX  
 SQ Sequence 721 AA;

Query Match 95.5%; Score 3530; DB 23; Length 721;  
 Best Local Similarity 92.6%; Pred. No. 0;  
 Matches 674; Conservative 0; Mismatches 14; Indels 40; Gaps 3;

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 Db 1 MLPRGRPRALGAAALLLLLLLLGFLFGGDLGCE-----RREPGRAGAPGCFPGPLM 53  
 Qy 53 TTAPTAARSRRR-----PPKCELLHVAIVCAGHNSSRDVI 87  
 | |||  
 Db 54 PRVPPDGRRLRAAALDGDPGAGPGDHNRSDCGPQPPPPKCELLHVAIVCAGHNSSRDVI 113  
 Qy 88 ILVKSMLFYRKNPLHLHLVTDVARNILETLFHTWMVPAVRVSFYHADQLKPQVSWIPNK 147  
 |||||  
 Db 114 TLVKSMLFYRKNPLHLHLVTDVARNILETLFHTWMVPAVRVSFYHADQLKPQVSWIPNK 173  
 Qy 148 HYSGLYGLMKLVLPALPAELARVIVLDTDVTFASDISELWALFAHFSDTQAIGLVENQS 207  
 |||||  
 Db 174 HYSGLYGLMKLVLPALPAELARVIVLDTDVTFASDISELWALFAHFSDTQAIGLVENQS 233  
 Qy 208 DWYLGNLWKNHRPWPALGRGFNTGVILLRLDRLRQAGWEQMWRLTARRELLSLPATSLAD 267  
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 Db 234 DWYLGNLWKNHRPWPALGRGFNTGVILLRLDRLRQAGWEQMWRLTARRELLSLPATSLAD 293  
 Qy 268 QDIFNAVIKEHPLVQRLPCVWNVQLSDHTLAERCYSEASDLKVIHWNSPKKLRVKNKHV 327  
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 Db 294 QDIFNAVIKEHPLVQRLPCVWNVQLSDHTLAERCYSEASDLKVIHWNSPKKLRVKNKHV 353

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Db	354	EFFRNFYLTTFLEYDGNLLRRELFVCPSQPPPGAEQLQQALQLDEEDPCFEFRQQQLTVH	413
Qy	388	RVHVTFLPHEPPPPRPHDVTLVQQLSMDRLQMLEALCRHWPGPMSLALYLTDAEAQQFLH	447
Db	414	RVHVTFLPHEPPPPRPHDVTLVQQLSMDRLQMLEALCRHWPGPMSLALYLTDAEAQQFLH	473
Qy	448	FVEASPVLAARQDVAYHVYREGPLYPVNQLRNVALAQALTPYVFLSDIDFLPAYSLYDY	507
Db	474	FVEASPVLAARQDVAYHVYREGPLYPVNQLRNVALAQALTPYVFLSDIDFLPAYSLYDY	533
Qy	508	LRASIEQLGLGSRKKAALVVPFETLRYRFSFPHSKVELLALLDAGTLYTFRYHEWPRGH	567
Db	534	LRASIEQLGLGSRKKAALVVPFETLRYRFSFPHSKVELLALLDAGTLYTFRYHEWPRGH	593
Qy	568	APTDYARWREAQAPYRVQWAANYEPYVVVPRDCPRYDPRFVGFGWNKVAHIVELDAQEYE	627
Db	594	APTDYARWREAQAPYRVQWAANYEPYVVVPRDCPRYDPRFVGFGWNKVAHIVELDAQEYE	653
Qy	628	LLVLPEAFTIHLPHAPSLDISRFRSSPTYRDCLQALKDEFHQDLSRHHGAAALKYLPALQ	687
Db	654	LLVLPEAFTIHLPHAPSLDISRFRSSPTYRDCLQALKDEFHQDLSRHHGAAALKYLPALQ	713
Qy	688	QPQSPARG	695
Db	714	QPQSPARG	721